

A

Ece1-V5	MKFSKIACATVFALSSQAIIHHAPEFNMKRDVAPAAPAAPADQAPTVPAPQEFNTAITK
Ece1	MKFSKIACATVFALSSQAIIHHAPEFNMKRDVAPAAPAAPADQAPTVPAPQEFNTAITK

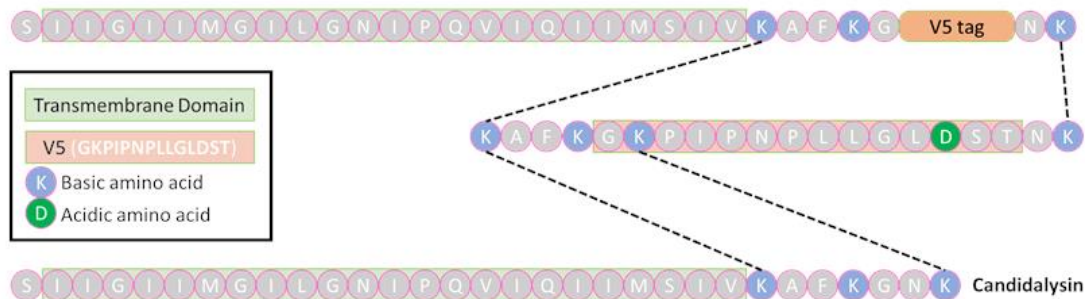
Ece1-V5	RSIIGIIMGILGNIPQVIQIIMSIVKAFKGKPIPNPLGLDSTNKREDIDSVVAGIAD
Ece1	RSIIGIIMGILGNIPQVIQIIMSIVKAFG-----NKREDIDSVVAGIAD

Ece1-V5	MPFVVRAVDTAMTSVASTKRDGANDDVANAVVRLPEIVARVATGVQQSIENAKRDGVDPV
Ece1	MPFVVRAVDTAMTSVASTKRDGANDDVANAVVRLPEIVARVATGVQQSIENAKRDGVDPV

Ece1-V5	GLNLVANAPRLISNVFDGVSETVQQAQRDGLDFLDELLQRLPQLITRSAESALKDSQPV
Ece1	GLNLVANAPRLISNVFDGVSETVQQAQRDGLDFLDELLQRLPQLITRSAESALKDSQPV

Ece1-V5	KRDAGSVALSNLIKKS IETVGIENAAQIVSERDISSLIEEYFGKA
Ece1	KRDAGSVALSNLIKKS IETVGIENAAQIVSERDISSLIEEYFGKA

B



S6 Fig. Protein sequence of Candidalysin-V5. (A) Sequence alignment of wild-type Ece1 and Ece1-V5. Candidalysin is highlighted in green, Kex1/2 cutting sites are highlighted in yellow, and the V5 sequence is indicated by red font. (B) Scheme of Candidalysin-V5. Basic and acidic amino acid are indicated.